

RESULT 1  
 VP26\_EBV

ID VP26\_EBV Reviewed; 176 AA.  
 AC P14348;  
 DT 01-JAN-1990, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JAN-1990, sequence version 1.  
 DT 24-JUL-2007, entry version 31.  
 DE Capsid protein VP26.  
 GN ORFNames=BFRF3;  
 OS Epstein-Barr virus (strain B95-8) (HHV-4) (Human herpesvirus 4).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Lymphocryptovirus.  
 OX NCBI\_TaxID=10377;  
 OH NCBI\_TaxID=9606; Homo sapiens (Human).  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=84270667; PubMed=6087149; DOI=10.1038/310207a0;  
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,  
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,  
 RA Tuffnell P.S., Barrell B.G.;  
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";  
 RL Nature 310:207-211(1984).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=86045997; PubMed=2998075; DOI=10.1016/0042-6822(85)90230-2;  
 RA Hudson G.S., Gibson T.J., Barrell B.G.;  
 RT "The BamHI F region of the B95-8 Epstein-Barr virus genome.";  
 RL Virology 147:99-109(1985).  
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 DR EMBL; V01555; CAA24838.1; ALT\_INIT; Genomic\_DNA.  
 DR EMBL; M11923; AAA45870.1; -; Genomic\_DNA.  
 DR InterPro; IPR009299; Herpes\_capsid.  
 DR Pfam; PF06112; Herpes\_capsid; 1.  
 PE 4: Predicted;  
 KW Capsid protein; Virion.  
 FT CHAIN 1 176 Capsid protein VP26.  
 FT /FTId=PRO\_0000115739.  
 SQ SEQUENCE 176 AA; 18147 MW; DAB605ED00F1A656 CRC64;

Alignment Scores:

Fred. No.:	5.43e-52	Length:	176
Score:	878.00	Matches:	176
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	88.1%	Indels:	0
DB:	1	Gaps:	0

US-10-036-729-1 (1-538) x VP26\_EBV (1-176)

Qy 5 ATGGCAGCCGGCTGCCCAAGCCACCCCTCCAGGGGAGGCTGGAGGCGGATTTCAGAC 64  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MetAlaArgArgLeuProLysProThrLeuGlnGlyArgLeuGluAlaAspPheProAsp 20  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 65 AGTCCCTGCTTCATAAATTTCAAGAGCTGAACAGATAATCTCCCCAATGATGTTTT 124

Db	21		SerProLeuLeuProLysPheGlnGluLeuAsnGlnAsnAsnLeuProAsnAspValPhe	40
Qy	125	CGGGAGGCTCAAAGAAGTTACCTGGTATTTCTGACATCCAGTTCGCTACGAAGAGTAC	184	
Db	41		ArgGluAlaGlnArgSerTyrLeuValPheLeuThrSerGlnPheCysTyrGluGluTyr	60
Qy	185	GTGCAGAGGACTTTTGGGGTGCTCGGCGCCAACGCGCCATAGACAAGAGGCAGAGAGCC	244	
Db	61		ValGlnArgThrPheGlyValProArgArgGlnArgAlaIleAspLysArgGlnArgAla	80
Qy	245	AGTGTGGCTGGGGCTGGTGCTCATGCACACCTTGGCGGGTCATCCGCCACCCCGTCCAG	304	
Db	81		SerValAlaGlyAlaGlyAlaHisAlaHisLeuGlyGlySerSerAlaThrProValGln	100
Qy	305	CAGGCTCAGGCGCGCATCCGCTGGGACCGGGGCTTGGGCATCATCAGCGCCGTCCACG	364	
Db	101		GlnAlaGlnAlaAlaAlaSerAlaGlyThrGlyAlaLeuAlaSerSerAlaProSerThr	120
Qy	365	GCCGTAGCCCACTCCGCGACCCCTCTGTTTCTTTCATCTATTAGCAGCCTCCGGGCCGCG	424	
Db	121		AlaValAlaGlnSerAlaThrProSerValSerSerSerIleSerSerLeuArgAlaAla	140
Qy	425	ACTTCGGGGGCGACTGCCGCCCTCCGCCCGCAGCCGTCGATACCGGGTCAGGTGGC	484	
Db	141		ThrSerGlyAlaThrAlaAlaAlaSerAlaAlaAlaAlaValAspThrGlySerGlyGly	160
Qy	485	GGGGGACAACCCACGACACCGCCACGCGGGGCACGTAAGAAACAG	532	
Db	161		GlyGlyGlnProHisAspThrAlaProArgGlyAlaArgLysLysGln	176